

1 GCTACGCGGGCCACGCTGCTGGCTGGCCTGACCTAGGCGCGCGGGGTCGGGCGGCCGCGCGGGCGGGCT
70 GAGTGAGCAAGACAAGACACTCAAGAAGAGCGAGCTGCGCCTGGGTCCCGGCCAGGCTTGACGCGAGAG
139 GCGGGCGGCAGACGGTGCCTGGCGGAATCTCTGAGCTCGGCGGCCAGCTCTGGTGCCAGCGCCAGT
208 GGCGCGCGCTTCGAAAGTGACTGGTGCCTCGCGCCCTCTCTCGGTGCGGGACCATGAAGCTGCTGCCG
M R L L P
1
277 TCGGTGGTGCTGAAGCTCTTTCTGGCTGCAGTTCTCTCGGCACTGGTGACTGGCGAGAGCCTGGAGCGG
S V V L K L F L A A V L S A L V T G E S L E R
10 20
346 CTTCCGAGAGGGCTAGCTGCTGGAACCAGCAACCCGGACCTCCCACTGTATCCACGGACCAGCTGCTA
L R R G L A A G T S N P D P P T V S T D Q L L
30 40 50
415 CCCCTAGGAGGCGGCGGGGACCGGAAAGTCCCTGACTTGCAAGAGGCAGATCTGGACCTTTTGAGAGTC
P L G G G R D R K V R D L Q E A D L D L L R V
60 70
484 ACTTTATCCTCCAAGCCACAAGCACTGGCCACACCAACAAGGAGGAGCACGGGAAAAGAAAGAGAAA
T L S S K P Q A L A T P N K E E H G K R K K K
80 90
553 GGCAAGGGGCTAGGGAAGAAGAGGGACCCATGTCTTCGGAAATACAAGGACTTCTGCATCCATGGAGAA
G R G L G K K R D P C L R K Y K D F C I B G E
100 110 120
622 TGCAAAATATGTGAAGGAGCTCCGGGCTCCCTCCTGCATCTGCCACCCGGGTTACCATGGAGAGAGGTGT
C K Y V R E L R A P S C I C H P G Y H G E R C
130 140
691 CATGGGCTGAGCCTCCAGTGGAATAATCGCTTATATACCTATGACCACACAACCATCCTGGCCGTGGTG
H G L S L P V E N R L Y T Y D H T T I L A V V
150 160
760 GCTGTGGTGCTGTCACTGTCTGTCTGCTGGTCACTCGTGGGGCTTCTCATGTTTAGGTACCATAGGAGA
A V V L S S V C L L V I V G L L M F R Y H R R
170 180
829 GGAGGTTATGATGTGGAATAATGAAGAGAAAGTGAAGTTGGGCATGACTAATTCCTCACTGA (SER ID NO:1)
G G Y D V E N E E K V K L G M T N S H (SER ID NO:2)
190 200

Fig. 1